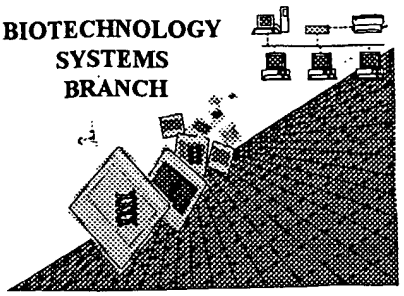
0913

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/943,531

Source: OIPE

Date Processed by STIC: 9/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/943,531

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/943,531

DATE: 09/20/2001
TIME: 13:40:18

Input Set : A:\GG119-2US.ST25.txt
Output Set: N:\CRF3\09202001\I943531.raw

pp 1-5

Does Not Comply
Corrected Diskette Needed

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  3 <110> APPLICANT: Risinger, Carl
  4       Andersson, Maria K.
  5       Lewander, Tommy K.
  6       Olaisson, Erik K.
  8 <120> TITLE OF INVENTION: Detection of CYP2C19 Polymorphisms
 10 <130> FILE REFERENCE: GG119.2US
 12 <140> CURRENT APPLICATION NUMBER: US/09/943,531
 12 <141> CURRENT FILING DATE: 2001-08-30
 12 <150> PRIOR APPLICATION NUMBER: GB 0021286.0
 13 <151> PRIOR FILING DATE: 2000-08-30
 15 <160> NUMBER OF SEQ ID NOS: 37
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
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 21 <212> TYPE: DNA
 22 <213> ORGANISM: homo sapiens
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 29 cccctctgca gtgatggaga agggagaact cttatttttt ctcatgagca tctctggggc    180
 31 tgttttcctt agataaataa gtggttctat ttaatgtgaa gcctgtttta tgaacaggat    240
 33 gaatgtggta tatattcaga ataactaakg tttggaagtt gttttgtttt gctaaaacaa    300
 35 agttttagca aacgattttt tttttcaaat ttgtgtcttc tgttctcaaa gyatctctga    360
 37 tgtaagagat aatgcgccac gatgggcatc agaagacctc agctcaaatc ccagttctgc    420
 39 cagctatgag ctgtgtggca ccaacaggtg tcctgttctc ccagggtctc cttttccca     480
 41 tttgaaatat aaaaaataac aattcctgcc ttcacgtgtt tttttagggg gttaaatggt    540
 43 aaaggtgttt atatctgcta aggtaattta cttgatatat gtttggttat tgaagatata    600
 45 tgagttatgt tagctatttc atgtttaggc tgctgtattt ttagtaggct atattaaata    660
 47 gaggatttca ttataaagga caaagtctcc taatcttcga tataggattg acatactttt    720
 49 taaatataca aggcatagaa tatggccatt tccgttaaat cataaattcc caactggtta    780
 51 ttaatctaag aattcagaat tttaagtaat tgtttttgca tcagattgtt tacttcagtg    840
 53 ctctcaatta tgacggtgca ttggaaccac ttgggttaac atttttttgt ttttattacc    900
 55 aatacctagg cttcaaccta gtacaatgaa accagaatgt acagagtggg cactgggacg    960
 57 aaggagaaca agaccaaagg acattttatt tttatctcta tcagtgggtc aaagtccttt   1020
 59 cagaaggagc atatagtggg cctaggtgat tggccactty atccatcaaa gaggcacaca   1080
 61 cacttaatta gcatggagtg ttataaaaag cttggagtgc aagctcacgg ttgtcttaac   1140
 63 aagaggagaa ggcttcaatg gatccttttg tggtccttgt gctctgtctc tcatgtttgc   1200
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 78 <211> LENGTH: 11
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all item 10 on Error Summary Sheet

RAW SEQUENCE LISTING DATE: 09/20/2001
PATENT APPLICATION: US/09/943,531 TIME: 13:40:18

Input Set : A:\GG119-2US.ST25.txt
Output Set: N:\CRF3\09202001\I943531.raw

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86 <210> SEQ ID NO: 4
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88 <212> TYPE: DNA
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125 <213> ORGANISM: synthetic
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131 <210> SEQ ID NO: 9
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140 <210> SEQ ID NO: 10
141 <211> LENGTH: 20
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145 <400> SEQUENCE: 10
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152 <213> ORGANISM: synthetic

RAW SEQUENCE LISTING DATE: 09/20/2001
PATENT APPLICATION: US/09/943,531 TIME: 13:40:18

Input Set : A:\GG119-2US.ST25.txt
Output Set: N:\CRF3\09202001\I943531.raw

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164 agtgggcact gggacga 17
167 <210> SEQ ID NO: 13
168 <211> LENGTH: 20
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170 <213> ORGANISM: synthetic
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176 <210> SEQ ID NO: 14
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179 <213> ORGANISM: synthetic
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191 tccatgctaa ttaagtgtgt gtg 23
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206 <213> ORGANISM: synthetic
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RAW SEQUENCE LISTING DATE: 09/20/2001
PATENT APPLICATION: US/09/943,531 TIME: 13:40:18

Input Set : A:\GG119-2US.ST25.txt
Output Set: N:\CRF3\09202001\I943531.raw

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239 <210> SEQ ID NO: 21
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250 <212> TYPE: DNA
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RAW SEQUENCE LISTING DATE: 09/20/2001
PATENT APPLICATION: US/09/943,531 TIME: 13:40:18

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Output Set: N:\CRF3\09202001\I943531.raw

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331 <212> TYPE: DNA
332 <213> ORGANISM: synthetic
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348 <211> LENGTH: 11
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356 <210> SEQ ID NO: 34
357 <211> LENGTH: 11
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370 <400> SEQUENCE: 35
371 gtttggaagt 10
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The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY DATE: 09/20/2001
PATENT APPLICATION: US/09/943,531 TIME: 13:40:19

Input Set : A:\GG119-2US.ST25.txt
Output Set: N:\CRF3\09202001\I943531.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date